

Fig. 1

A

Selection of candidate SM synthases from the animal database
266,504 entries searched (06/02)

- 1) LPP motif: H-Φ-x₂-D-b-x₂-n-X₃-n
- 2) Biochemical function unknown
- 3) No homologues in yeast
- 4) >2 transmembrane domains

BLAST search

31 candidate SM synthase sequences
human (9), mouse (9), worm (9), fly (4)

B

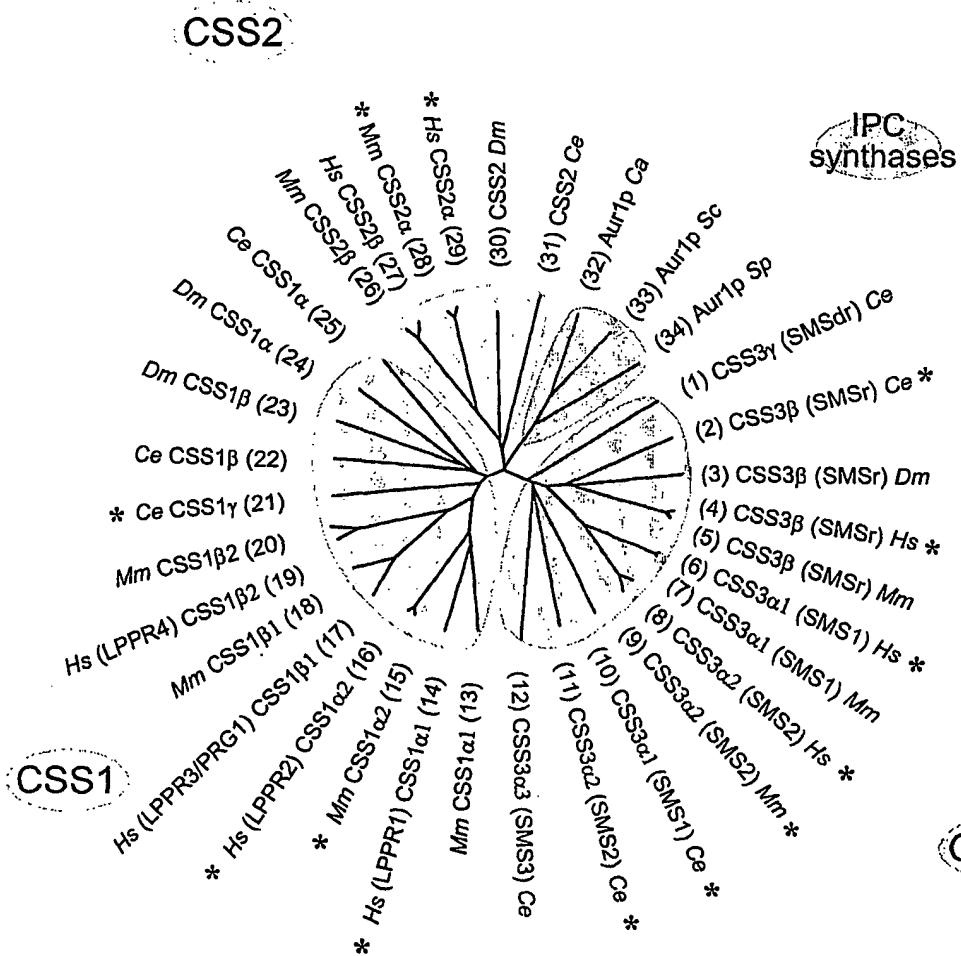
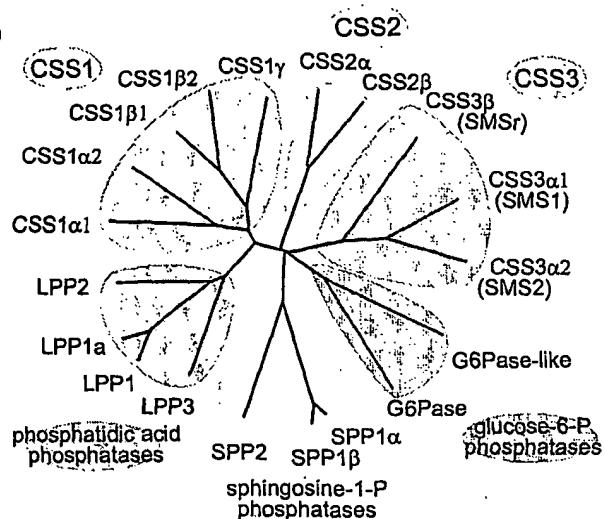


Fig. 2

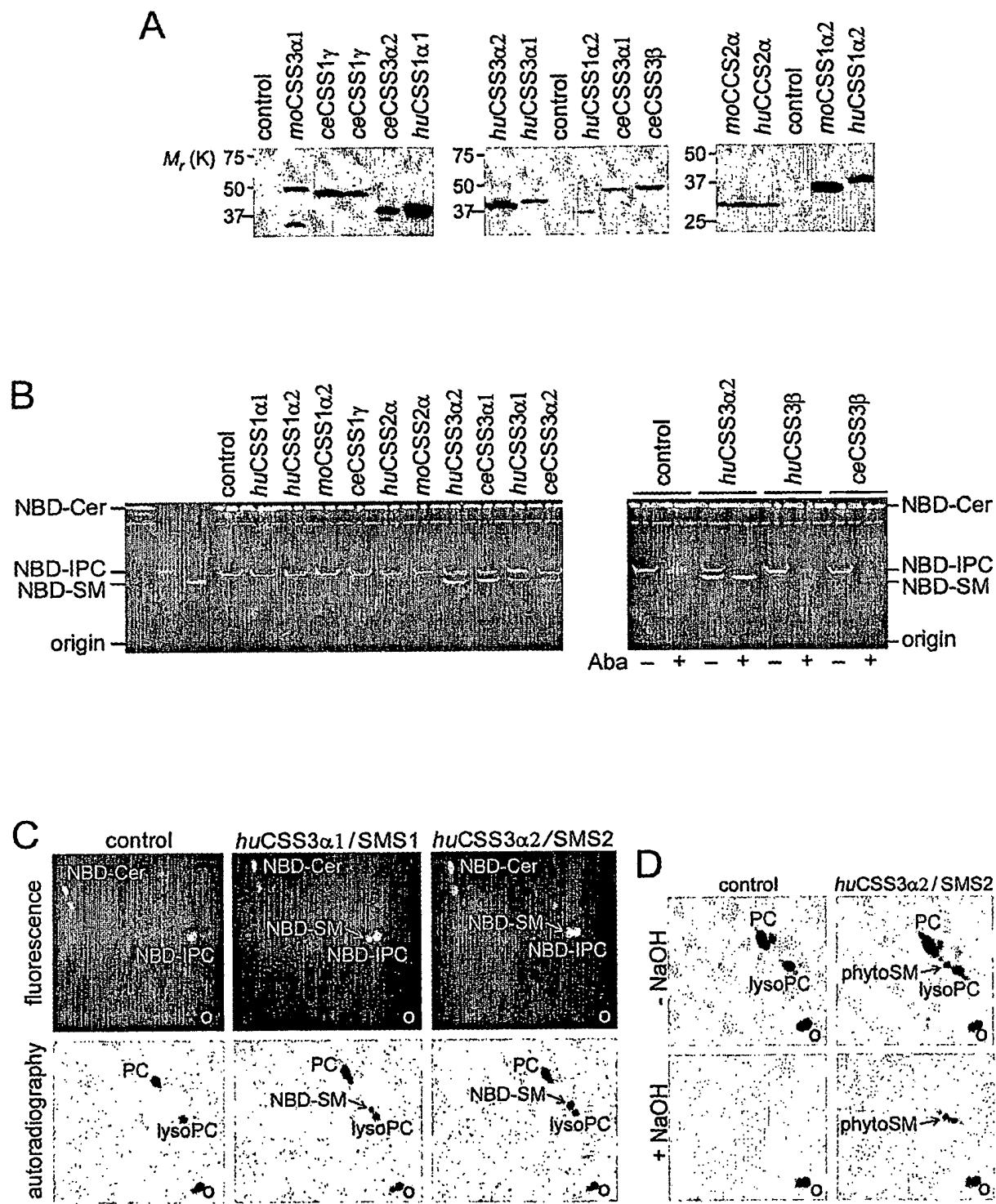


Fig. 3

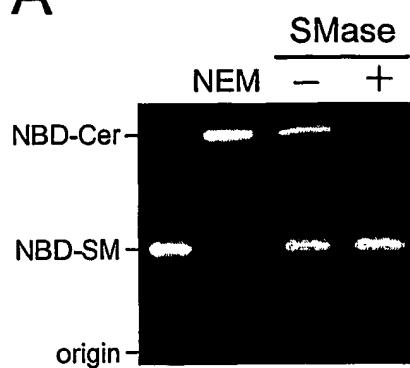
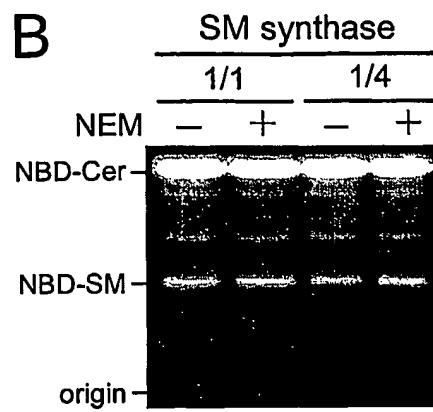
A**B**

Fig. 4

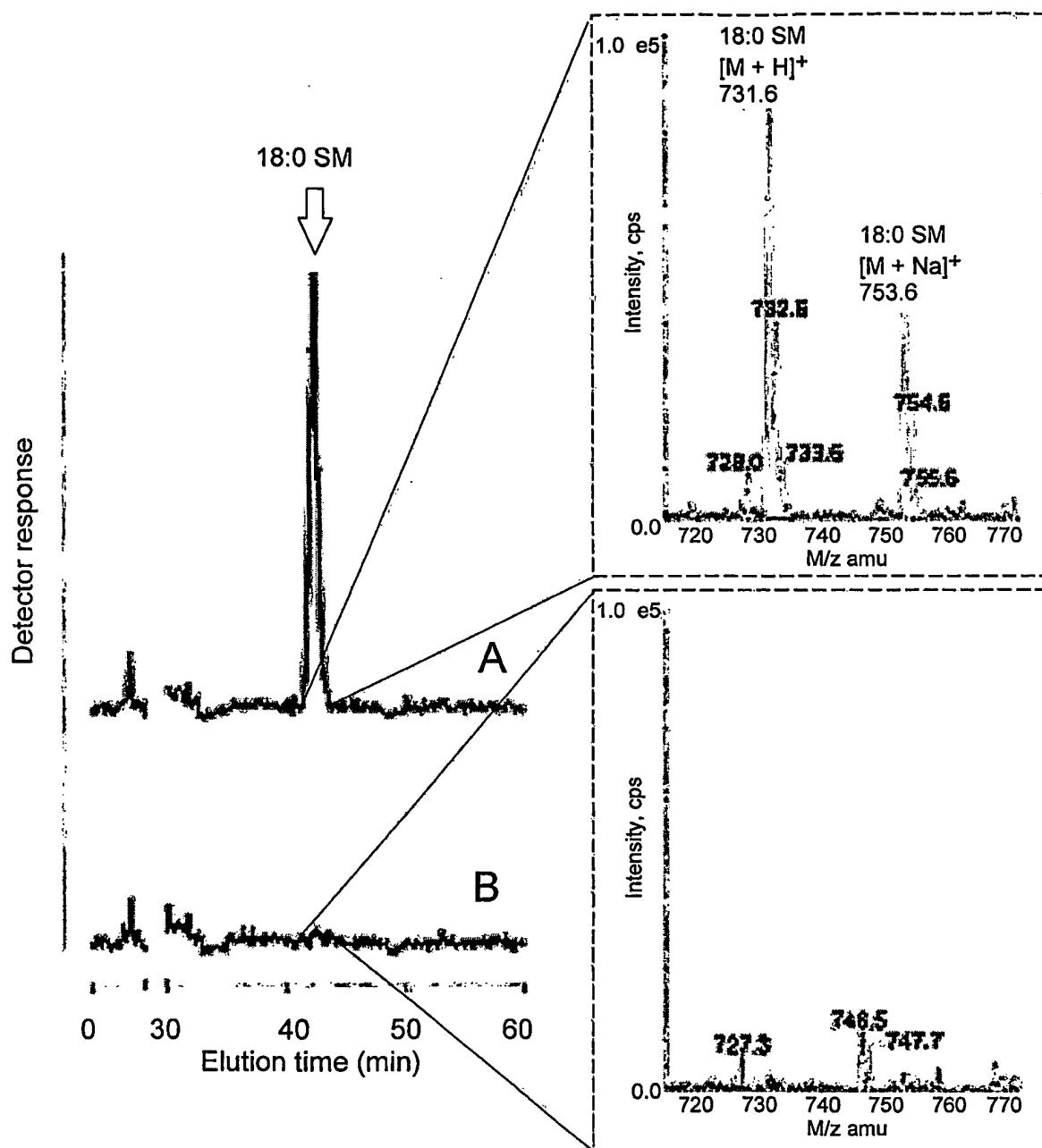
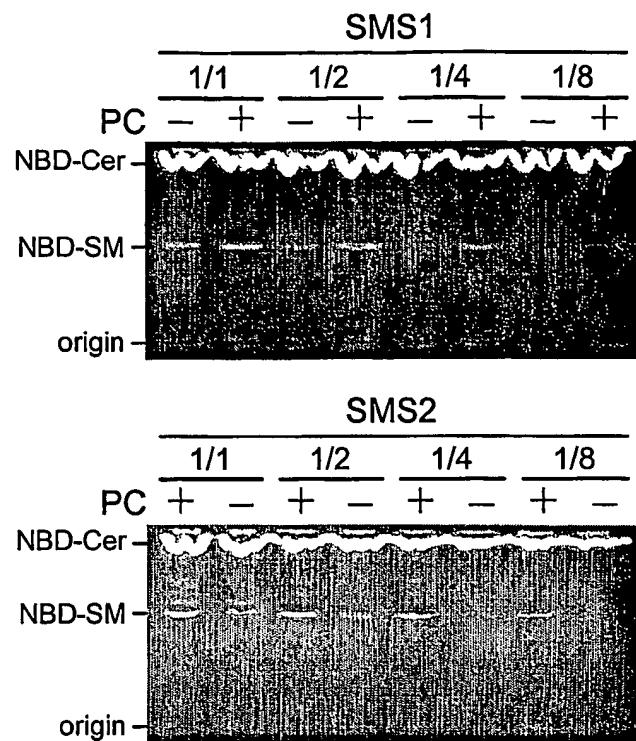
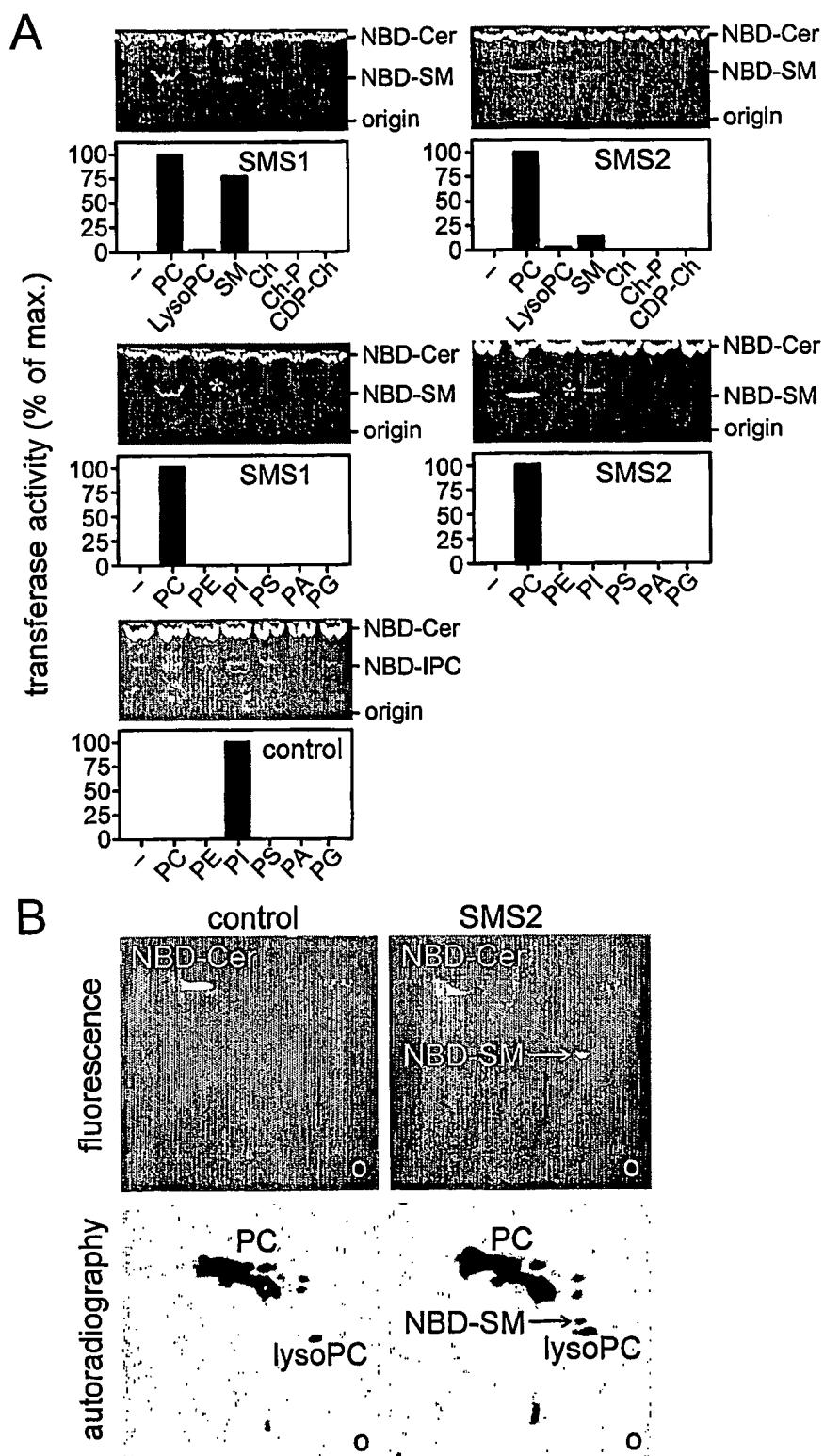


Fig. 5

6/13

Fig. 6



7/13

Fig. 7

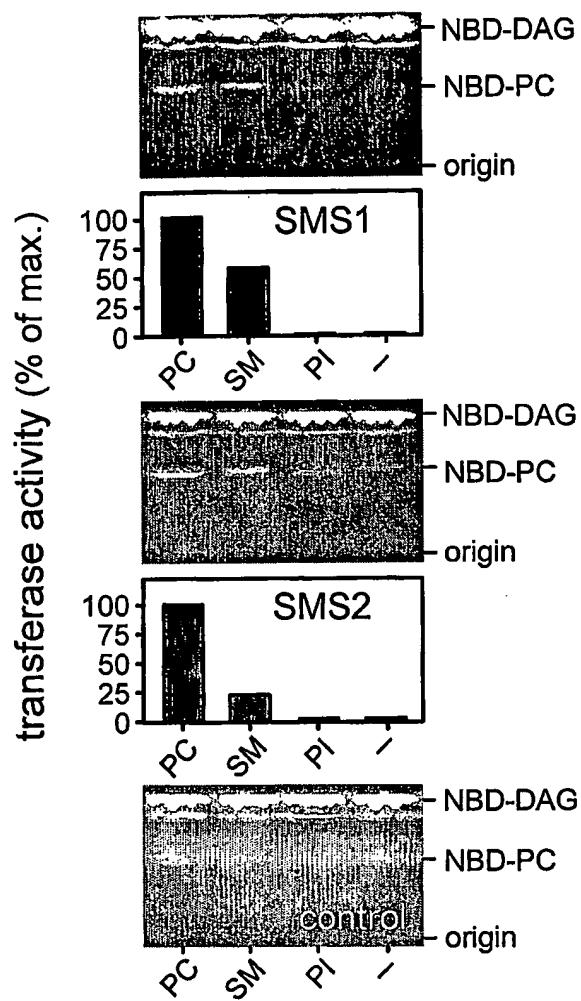


Fig. 8

A

Hs SMS1 1 MKEVYYWSPKKVADWLEENAMPEYCEPLE --- HFTGQDLINLTQEDFKKPLCRVSSDNG
Hs SMS2
Hs SMSr 1 MAGPNQLCIRRWTTKHAVWLKDGGFFEYVDILCNKHLRDGITALTLEYDLSPPLEIKVLGD

Hs SMS1 58 QRLUDMIETLKMEEHH --- LEAH --- KNGHANGHNLN --- GVDIPTPDGSFSIKIKPNG-MPNGYRK -
Hs SMS2 1 MDIETAKLEEH --- LENQ --- RSDPTNTYARPAEPVEEENKNGNGKPKSLSSG-LRKGTKKY
Hs SMSr 66 KRLMLSVRKLQKIHIDVLEEMGYNSDSPMGSMTPFISALQSTDWLNGEISHDCDGPIIDLNSDQ

TM1 -D1-

Hs SMS1 114 EMIKIPMPEELERSQYPMEWGKTFLAFLYALSCFVLTVMISVVHERVPPKEVQPLPDTFFDHF
Hs SMS2 56 PDIYJGIAMPTESRNKFPIEWWKWTGIAFIYAVFNLVLTVMITVVHERVPPKELSPPLPDKFFDY
Hs SMSr 131 YQYMMNGKNKHSVRRLDP-EYWKTILSCIYVFIVFGFTSFIMVIVHERVPDMQTYPPLPDIFLDSV

TM2 D2-TM3-

Hs SMS1 178 NRVOWAFSICEINGMILVGLWLQWLKYKSIJSRRFFCIVGTLILYRCLTMYVTTLPVPGMHF
Hs SMS2 122 DRVKWAFSVSEINGILVGLWITQWLFLRYKSIVGRRFCIIIGTLILYRCLTMYVTTLPVPGMHF
Hs SMSr 196 PRTPWAFAMTEVCGMILCYIWLLVLLHKHRSILLRRLCSLMGTVELLRCFTMFTSLSPVGQH

D3 TM4

Hs SMS1 243 NCSPKLFGDWEAQQLRRIMKLIAAGGGLSITGSHNMCGDYLYSGHTVMLTLTYLFKEYSPRRLWWY
Hs SMS2 187 QCAPKLNQDSQAKVQRILRLISGGGLSITGSHICGDFLFSGHTVLTLYLFKEYSPRHFWWY
Hs SMSr 260 QCTGKIYGSVWEKLHRAFAWSFGMTLTGVH-TCDYMFSGHTVVLTMNLNFVTEYTPRSWNFL

TM5 D4-TM6

Hs SMS1 309 HWICWLLSVVGIFCILLAHDHYTVDVYVAYYITTRLFWWYHTMANQQVLKEASQMNLARVWWYR
Hs SMS2 252 HLIICWLLSAAGIICILVAHEHYTDVIIAYYITTRLFWWYHSMANEKNLKVSSQTNFLSRAWWF
Hs SMSr 324 HTLSWVLNLFGIFFILAAHEHYSIDVFIAGYITTRLFLYYHTLANTR---AYQQSRRARIW-PP

Hs SMS1 373 PFQYFEKVNQGIVPRSYHWFPWPW-VVHLSRQVKYSRLVNDT
Hs SMS2 317 IFYFFFENQGSIPCCESWPILSWPPGCFKSSCKKYSRQKIGEDNEKST
Hs SMSr 384 MFSFEEECNVNGTVRNEYCWPFESKPAIKRLIG

B

	-D1-	D2	D3	D4
Hs SMS1	168 PLPD	213 RRFFCIVGTLILYRCLTMYVT	277 CGDYIYSGHT	328 HYTVDVVVAYYITTRLFWWYH
Hs SMS2	112 PLPD	157 RRFCFILGTLYLRYCITTMVY	221 CGDFLFSGHT	272 HYTIDVIIAYYITTRLFWWYH
Ce SMS1	175 PLPD	220 RRLCFIGSILYGMRCITMMV	288 CGDYIYSGHT	339 HYTIDVILSYFACTRTRVFWAYH
Ce SMS2	88 PLPD	133 RRTFLILGAIMYGLRAVILGVT	202 CGDLMSGHT	253 HYTMDVLLAYWLTHVFWASH
Ce SMS3	65 SLPD	110 KRVVFCAGTLYAMRSVTLAAT	175 CGDLLFSGHT	226 HYTIDVILAYWLSNMVFRMYH
Pf SMS1	161 PLKD	211 IRIILLLSFIYCYCIRSFFIYVT	266 CTDLVYSGHT	315 HYTVDVLMGYVFGGSVFLFYH
Pf SMS2	112 PLSD	161 CRFLYIVGSFYIIRGLLIVYVT	216 CADLIVSGHT	265 HYTSDVLLGIIFGVFMFSFYH
Hs SMSr	185 PLPD	230 RRLCSLMGTVELLRCFTMELT	293 CGDYMFSGHT	344 HYSIDVFIAYITTRLFLYYH
Dm SMSr	232 PLPD	277 RRFFALAGTVELLRCFTMELT	350 CGDYMFSGHT	401 HYSIDVFAAYITSRFLFLYYH
Ce SMSr	214 PLPD	259 RRMFSIILGTVELLRCFTMELT	322 CGDYMFSGHT	373 HYSIDVFIAYISSRMFLFLYYH
Ce SMSdr	111 PLPD	183 RRVEFCLAMAYSFRAICVTLIF	247 CGDLIVSGHT	298 HYMIDIVLGYTYSIRIFMEYH
<u>consensus</u>	PLPD	RRxxxxbxnxnbΦxxRxxxxbxbt	CGDxbxSGHT	HYTbDVbΦxxnnxbFxxYH

9/13

Fig. 10

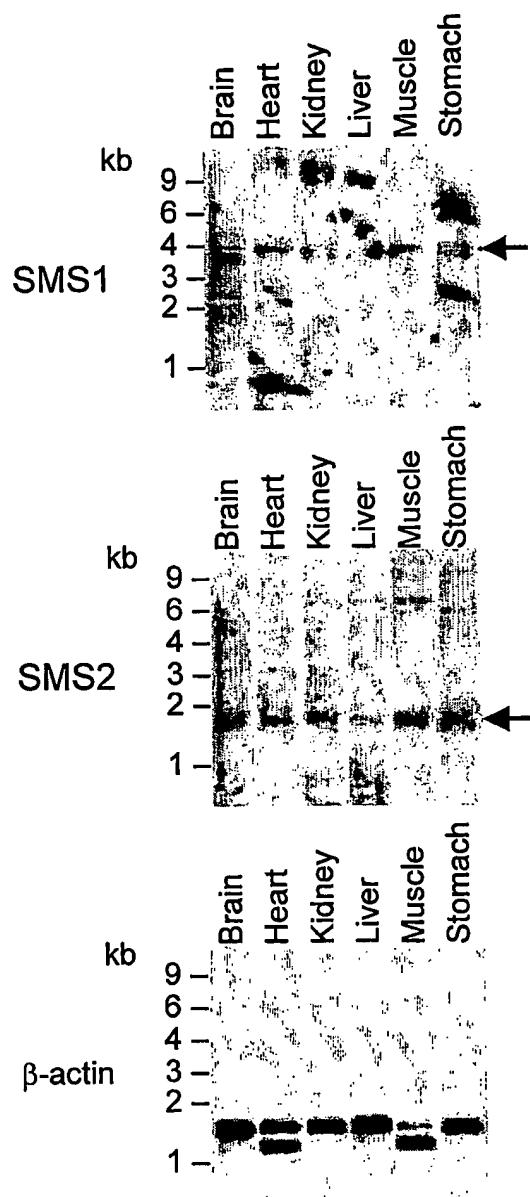


Fig. 11

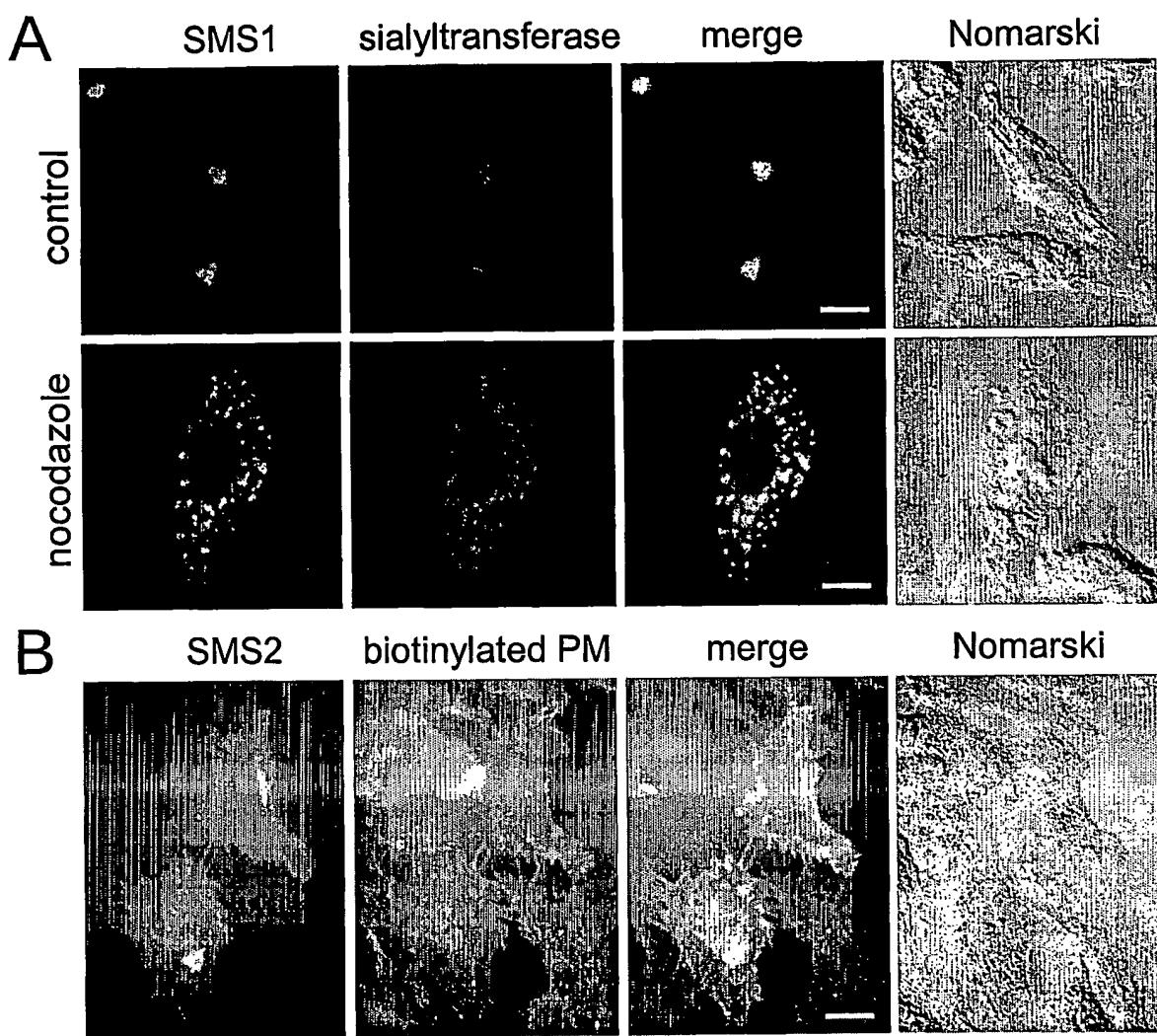


Fig. 12

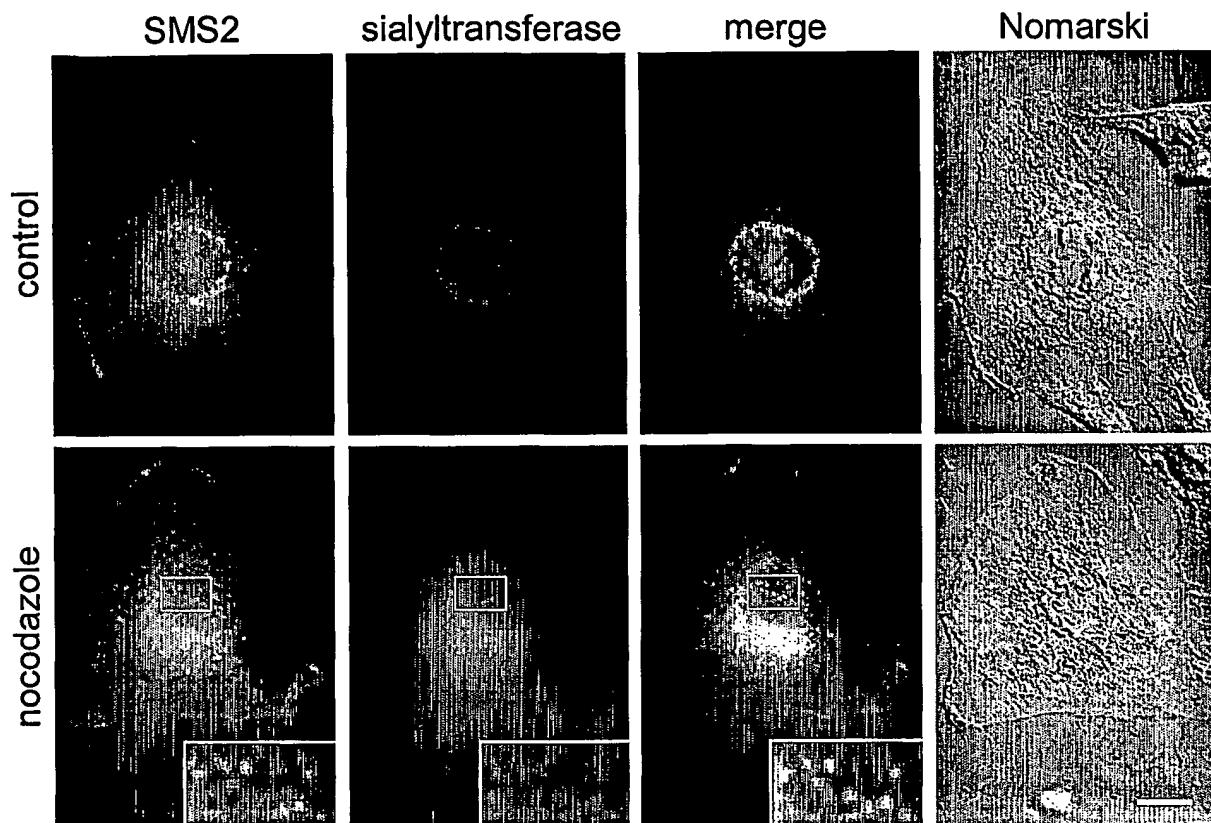
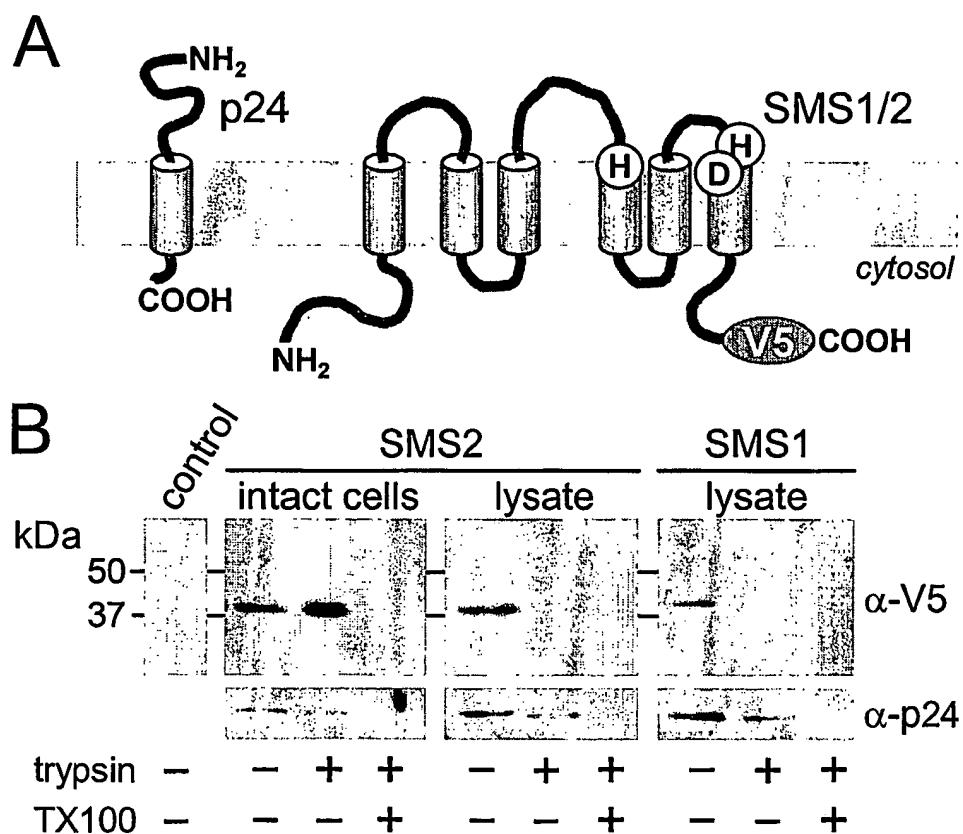


Fig. 13



13/13

Fig. 14

